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EXAMINER	
THOMAS, DAVID C	

ART UNIT	PAPER NUMBER
1637	

DATE MAILED: 11/27/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/731,419	BEJJANI ET AL.	
	Examiner	Art Unit	
	David C. Thomas	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *21 September 2006*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,2,4,5,7-9,11,16,21-23,51-53 and 71-74* is/are pending in the application.

4a) Of the above claim(s) *51-53* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,2,4,5,7-9,11,16,21-23, and 71-74* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *11 July 2006*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

1. Applicant's amendment filed September 21, 2006 is acknowledged. Claims 1, 2, 4, 5, 7-9, 11, 16, 21-23 and 71 (currently amended), and claims 72-74 (original), will be examined on the merits. Claims 51-53 were previously withdrawn as a non-elected invention. Claim 28 has been canceled.

Claim Rejections - 35 USC § 102

2. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

3. Claims 1, 2, 4, 5, 7-9, 11, 16, 21-23, and 71-74 are rejected under 35 U.S.C. 102(b) as being anticipated by Chenchik et al. (U.S. Patent No. 5,759,822).

Chenchik teaches a method of creating a pure clinical reference solution for testing multiple genetic conditions (for use as positive or negative control reactions, column 11, lines27-28, to test for conditions such as chromosome aberrations including point mutations, deletions, insertions, transversions and other conditions, column 13, lines 2-8), wherein the clinical reference solution is substantially free of clinically irrelevant nucleic acid detrimental to the testing (fragments corresponding to cDNA can be prepared free of the poly A-minus fractions or other genomic impurities, column 24, lines 8-12), comprising:

determining one or more clinically relevant sites on one or more nucleic acid sequences (fragments can be used to map chromosome aberrations in genomic DNA, column 12, line 66 to column 13, line 8);

for each clinically relevant site, designing an arrangement of bases to emulate the clinically relevant site as isolated from adjacent clinically irrelevant nucleic acid (fragments corresponding to cDNA can be prepared free of the poly A-minus fractions or other genomic impurities, column 24, lines 8-12), wherein the arrangement of bases also includes one or more primer targets (after preparation total cDNA, an adaptor is ligated to one end each cDNA, column 24, line 15-17);

synthesizing, base by base, a single-stranded artificial version of each arrangement of bases associated with each clinically relevant site (fragments were amplified using unique priming site and a polyA primer, column 24, lines 18-22); and

mixing each artificial version of a clinically relevant site into a single solution (Figure 3, top, two different fragments are mixed and using same primer sets and adaptors, result in amplification of each containing adaptors, Figure 3 bottom left; also described in column 13, lines 9-29; fragments can be cloned into a plasmid or other vector for use a reference, column 12, line 66 to column 13, line 2).

With regard to claim 2, Chenchik teaches a method wherein each clinically relevant site comprises a mutation of a normal human nucleic acid sequence, each mutation representing a human genetic condition (fragments made from cDNA can be used to test for conditions such as chromosome aberrations including point mutations, deletions, insertions, transversions and other conditions, column 13, lines 2-8).

With regard to claim 4, Chenchik teaches a method wherein:

the synthesizing one or more primer targets includes attaching a first sequence of nucleotides base by base to a first end of each of the one or more synthesized arrangements of bases (attachment of adaptor to serve as priming site, Figure 1, second line, left side), wherein the first sequence is complementary to a nucleotide sequence of a first primer of a primer set (primers complementary to adapters are added, column 14, lines 5-6), and

the synthesizing one or more primer targets includes attaching a second sequence of nucleotides base by base to a second end of each of the one or more synthesized arrangements of bases (attachment of adaptor to serve as priming site for second primer, Figure 1, second line, left side), wherein the second sequence is identical to a nucleotide sequence of a second primer of a primer set (primers complementary to adapters are added, column 14, lines 5-6).

With regard to claim 5, Chenchik teaches a method wherein the synthesizing comprises synthesizing, base by base, two complementary nucleic acid strands (by amplification using sequence-specific PCR primers, column 11, lines 62-67), wherein:

a first strand includes an artificial version of one of the clinically relevant sites and a nucleic acid tag complementary to a first primer of a primer set (composed of PCR-generated fragment, column 11, lines 62-67, with adapter added by ligation, column 13, lines 12-15 and lines 53-56 and Figure 1, second line), and

a second strand is complementary to the first strand and to a nucleic acid tag complementary to a second primer of a primer set (second strand of fragment obtained

as PCR product, column 11, lines 62-67, with adapter added by ligation, column 13, lines 12-15 and lines 53-56 and Figure 1, second line).

With regard to claim 7, Chenchik teaches a method wherein designing an arrangement of bases includes recreating a site of a mutation of a nucleotide in a normal human nucleic acid (fragment can be designed for using to test for conditions such as chromosome aberrations including point mutations, deletions, insertions, transversions and other conditions, column 12, line 66 to column 13, line 8), exclusive of extraneous nucleic acid material adjacent to the site of the mutation (fragments corresponding to cDNA can be prepared free of the poly A-minus fractions or other genomic impurities, column 24, lines 8-12).

With regard to claim 8, Chenchik teaches a method wherein:

each of the artificial versions of a clinically relevant site has an associated primer set (primers complementary to adapters are added, column 14, lines 5-6; Figure 3, both mixtures use primers a and b), and wherein:

the reference solution is tuned for a specific battery of clinical tests by differentially amplifying the different clinically relevant sites to different concentrations in the reference solution (unique cDNAs containing different adaptors at each end will yield roughly equal, but not identical, concentrations, in an amplification, column 13, lines 39-43).

With regard to claim 9, Chenchik teaches a method wherein different groups of the artificial versions of the clinically relevant sites in the reference solution have associated primer sets such that each different group of clinically relevant sites is

amplified independently (combining of mixtures and controlling amplification depending on formation of pan structures due to different fragments having either sites for a and b primers or only one primer, Figure 2, third section and bottom and column 13, line 67 to column 14, line 9).

With regard to claim 11, Chenchik teaches a method wherein independently amplifying each of the groups of clinically relevant sites includes controlling a physical characteristic of the reference solution to favor an amplification capability of one primer set over an amplification capability another primer set (primer set a or b is prevented from binding to one mixture which forms pan structure, but a and b effectively binds to o mixture containing both primer binding sites, column 14, lines 7-9, and Figure 2, bottom).

With regard to claim 16, Chenchik teaches a method further comprising adding normal human nucleic acid to the base by base synthesized artificial versions of the clinically relevant sites in order to achieve a mixture of the nucleic acids in the reference solution representing at least a segment of homologous heterozygous alleles (use of human skeletal muscle cDNA will include normal DNA, which is then used for library construction by adaptor ligation and PCR, Example 4, column 24, lines 5-25).

With regard to claim 21, Chenchik teaches a method further comprising joining two parts of one of the arrangements of bases together using a ligation extension to perform the synthesizing of a large arrangement of bases (ligation of adaptors to extend fragment ends, column 13, lines 12-15 and lines 53-56).

With regard to claim 22, Chenchik teaches a method further comprising using a bridge nucleic acid to join multiple parts of the arrangement of bases (one strand of double-stranded adaptor serves as bridge to ligate second strand of adaptor to fragment by increasing efficiency of ligation to dsDNA, Figure 1, second line, column 8, lines 22-24).

With regard to claim 23, Chenchik teaches a method further comprising using an overlap extension to join multiple parts of the arrangement of bases (using adaptors of unequal length which can be extended to fill in ends after annealing of strands using a DNA polymerase, Figure 2, steps 2 and 3 and column 8, lines 3-12).

With regard to claim 71, Chenchik teaches a method, comprising:

designing multiple reference nucleic acids (such as a cDNA library cloned into a vector, column 12, line 66 to column 13, line 2), wherein each reference nucleic acid comprises an arrangement of bases emulating a clinically relevant site of a human nucleic acid (fragments may contain sequences used for mapping chromosome aberrations, column 13, lines 2-8) exclusive of clinically irrelevant human nucleic acid adjacent to the clinically relevant site (fragments corresponding to cDNA can be prepared free of the poly A-minus fractions or other genomic impurities, column 24, lines 8-12);

synthesizing, base by base for each reference nucleic acid, a first mixture of various of the reference nucleic acids, wherein each of the various reference nucleic acids in the first mixture includes one or more tags allowing PCR amplification of the first mixture via a primer set specific to the tags of the first mixture (Figure 3, top, two

mixtures using same primer sets and adaptors, resulting in two populations of amplified products, Figure 3, bottom); and

synthesizing, base by base for each reference nucleic acid, a second mixture of various of the reference nucleic acids, wherein each of the various reference nucleic acids in the second mixture includes one or more tags allowing PCR amplification of the second mixture via a second primer set specific to the tags of the second mixture (Figure 3, top, two mixtures using same primer sets and adaptors, resulting in two populations of amplified products, Figure 3, bottom).

With regard to claim 72, Chenchik teaches a method, further comprising combining the first and second mixtures to make a single mixture and differentially amplifying the first mixture and the second mixture in a PCR reaction by controlling amounts of the first primer set and second primer set in the single mixture (amounts of primers are kept at equal levels, but prevented from binding to pan structures, thus leading to differential amplification of the mixtures, Figure 3 and column 14, lines 5-20).

With regard to claim 73, Chenchik teaches a method, wherein at least some of the reference nucleic acids include mutations of a normal human nucleic acid (partially homologous sequences, column 12, lines 28-30 or those with mutations, column 12, line 66 to column 13, line 8; see Example 4 for example of human nucleic acid, skeletal muscle, column 24, lines 8-25).

With regard to claim 74, Chenchik teaches a method, further comprising adding normal human nucleic acid to the single mixture to obtain heterozygous pairs, wherein each heterozygous pair includes a normal segment of human nucleic acid and a

mutated copy of the normal segment of human nucleic acid (normal genomic sequences analyzed along with mutant sequences for chromosome mapping, column 12, line 66 to column 13, line 8 and Example 4 for example of human nucleic acid, skeletal muscle, column 24, lines 8-25).

4. Claims 1, 2, 4, 5, 7-9, 11, 16, 21-23, and 71-74 are rejected under 35 U.S.C. 102(a) as being anticipated by Gordon et al. (U.S. Patent No. 6,607,911).

Gordon teaches a method of creating a pure clinical reference solution for testing multiple genetic conditions (such as multiple and distinct mutations in a gene, column 16, lines 29-32), wherein the clinical reference solution is substantially free of clinically irrelevant nucleic acid detrimental to the testing (fragments of control DNA construct used as reference standard may contain, for example, only exons and their intronic borders from cystic fibrosis transmembrane conductance regulator (CFTR) gene, each with associated mutant, column 16, lines 26-32), comprising:

determining one or more clinically relevant sites on one or more nucleic acid sequences (fragments used to construct control DNA can comprise exons of single gene or multiple genes of interest from one or multiple organisms for a given disease or disorder, column 18, lines 36-65);

for each clinically relevant site, designing an arrangement of bases to emulate the clinically relevant site as isolated from adjacent clinically irrelevant nucleic acid (fragments comprise exons of gene of interest, column 18, lines 38-40), wherein the arrangement of bases also includes one or more primer targets (one or more primer

sites were added to cassettes that also include unique restriction sites, column 23, lines 52-59);

synthesizing, base by base, a single-stranded artificial version of each arrangement of bases associated with each clinically relevant site (fragments containing cassettes were amplified using unique priming sites, column 23, line 60 to column 24, line 3; fragments can also be made chemically or by other means, column 22, lines 30-37); and

mixing each artificial version of a clinically relevant site into a single solution (cassettes were individually ligated into pGEM-T plasmids, column 24, lines 44-50).

With regard to claim 2, Gordon teaches a method wherein each clinically relevant site comprises a mutation of a normal human nucleic acid sequence (as measured in a Clinical Laboratory, column 6, lines 50-62), each mutation representing a human genetic condition (such as deltaF508 and delta1507 in exons 10 and 11, respectively, in human CFTR gene, column 3, lines 12-27 and column 16, lines 29-32).

With regard to claim 4, Gordon teaches a method wherein:

the synthesizing one or more primer targets includes attaching a first sequence of nucleotides base by base to a first end of each of the one or more synthesized arrangements of bases, wherein the first sequence is complementary to a nucleotide sequence of a first primer of a primer set (BssH II restriction site was incorporated on 5' end of exon 10 used in making DNA control construct, and contained priming site for amplification, column 23, line 52 to column 24, line 3), and

the synthesizing one or more primer targets includes attaching a second sequence of nucleotides base by base to a second end of each of the one or more synthesized arrangements of bases, wherein the second sequence is identical to a nucleotide sequence of a second primer of a primer set (Csp45 I restriction site was incorporated on 3' end of exon 10 used in making DNA control construct, and contained priming site for amplification, column 23, line 52 to column 24, line 3).

With regard to claim 5, Gordon teaches a method wherein the synthesizing comprises synthesizing, base by base, two complementary nucleic acid strands (strands are synthesized by PCR, column 23, line 60 to column 24, line 3), wherein:

a first strand includes an artificial version of one of the clinically relevant sites and a nucleic acid tag complementary to a first primer of a primer set (first strand of DNA control construct contains exon 10 or 11 and a unique mutation, and also has priming site on 5' end, column 23, lines 52-59), and

a second strand is complementary to the first strand and to a nucleic acid tag complementary to a second primer of a primer set (second strand of DNA control construct contains exon 10 or 11 and a unique mutation, and also has priming site on 3' end, column 23, lines 52-59).

With regard to claim 7, Gordon teaches a method wherein designing an arrangement of bases includes recreating a site of a mutation of a nucleotide in a normal human nucleic acid (such as deltaF508 and deltaI507 in exons 10 and 11, respectively, in human CFTR gene, column 3, lines 12-27 and column 16, lines 29-32), exclusive of extraneous nucleic acid material adjacent to the site of the mutation

(mutation sites are in exons only, and thus free of introns or other irrelevant nucleic acid material, column 18, lines 36-41).

With regard to claim 8, Gordon teaches a method wherein:

each of the artificial versions of a clinically relevant site has an associated primer set (primer set for exon 10, for examples, uses primers that bind in unique BssH II and Csp45 I restriction sites, column 23, lines 52-65), and wherein:

the reference solution is tuned for a specific battery of clinical tests by differentially amplifying the different clinically relevant sites to different concentrations in the reference solution (different concentrations of serial dilutions of plasmid containing DNA control construct were amplified using biotin-labeled primers for a set amount of cycles and added to microplate containing samples for hybridization and quantification, column 31, line 28 to column 32, line 28).

With regard to claim 9, Gordon teaches a method wherein different groups of the artificial versions of the clinically relevant sites in the reference solution have associated primer sets such that each different group of clinically relevant sites is amplified independently (unique primer sets can be used in a construct containing cassettes for exons 10 and 11 to amplify each independently, column 23, line 60 to column 24, line 25).

With regard to claim 11, Gordon teaches a method wherein independently amplifying each of the groups of clinically relevant sites includes controlling a physical characteristic of the reference solution to favor an amplification capability of one primer set over an amplification capability another primer set (exon 11 cassette PCR reactions

amplified the target more efficiently using shorter extension times, than the reactions of exon 10 cassette, which required longer extension times while still generating lower product yields, column 24, lines 4-25) .

With regard to claim 16, Gordon teaches a method further comprising adding normal human nucleic acid to the base by base synthesized artificial versions of the clinically relevant sites in order to achieve a mixture of the nucleic acids in the reference solution representing at least a segment of homologous heterozygous alleles (mixture of DNA control construct can contain fragments that comprise wild-type sequence of interest and as many mutations and variations as desired, column 20, lines 48-51 and column 24, lines 26-42; mutations were added by site directed mutagenesis, column 27, lines 19-22).

With regard to claim 21, Gordon teaches a method further comprising joining two parts of one of the arrangements of bases together using a ligation extension to perform the synthesizing of a large arrangement of bases (two or more fragments may be ligated together, each containing unique sites at their termini and wherein each site overlaps the adjacent or flanking site, in order to produce larger construct containing multiple cassettes, column 17, lines 1-11).

With regard to claim 22, Gordon teaches a method further comprising using a bridge nucleic acid to join multiple parts of the arrangement of bases (ends of fragments can be modified to form sticky ends to facilitate ligation to each other, column 18, lines 2-4).

With regard to claim 23, Gordon teaches a method further comprising using an overlap extension to join multiple parts of the arrangement of bases (exon 10 and 11 cassettes were joined together after digestion by ligation using their common restriction sites and A overhangs, column 24, lines 47-50 and column 26, lines 19-30).

With regard to claim 71, Gordon teaches a method, comprising:

designing multiple reference nucleic acids (separate constructs containing mutations such as deltaF508 and deltaI507 in exons 10 and 11, respectively, in human CFTR gene, column 3, lines 12-27 and column 16, lines 29-32), wherein each reference nucleic acid comprises an arrangement of bases emulating a clinically relevant site of a human nucleic acid exclusive of clinically irrelevant human nucleic acid adjacent to the clinically relevant site (fragments of control DNA construct used as reference standard may contain, for example, only exons and their intronic borders from cystic fibrosis transmembrane conductance regulator (CFTR) gene, each with associated mutant, column 16, lines 26-32);

synthesizing, base by base for each reference nucleic acid, a first mixture of various of the reference nucleic acids (fragment containing cassette for first reference site was amplified using unique priming sites, column 23, line 60 to column 24, line 3; fragment can also be made chemically or by other means, column 22, lines 30-37), wherein each of the various reference nucleic acids in the first mixture includes one or more tags allowing PCR amplification of the first mixture via a primer set specific to the tags of the first mixture (one or more primer sites for PCR were added to the cassette that also include unique restriction sites, column 23, lines 52-59); and

synthesizing, base by base for each reference nucleic acid, a second mixture of various of the reference nucleic acids (fragment containing cassette for second reference site was amplified using unique priming sites, column 23, line 60 to column 24, line 3; fragment can also be made chemically or by other means, column 22, lines 30-37), wherein each of the various reference nucleic acids in the second mixture includes one or more tags allowing PCR amplification of the second mixture via a second primer set specific to the tags of the second mixture (one or more primer sites for PCR were added to the cassette that also include unique restriction sites, column 23, lines 52-59).

With regard to claim 72, Gordon teaches a method further comprising combining the first and second mixtures to make a single mixture (cassettes were individually ligated into pGEM-T plasmids, column 24, lines 44-50) and differentially amplifying the first mixture and the second mixture in a PCR reaction by controlling amounts of the first primer set and the second primer set in the single mixture (primer amounts for the two primer sets were both used at 1.2 mM, column 31, lines 47-48, which generated different yields of exon 10 and 11 products, column 24, lines 12-25).

With regard to claim 73, Gordon teaches a method wherein at least some of the reference nucleic acids include mutations of a normal human nucleic acid (such as deltaF508 and deltaI507 in exons 10 and 11, respectively, in human CFTR gene, column 3, lines 12-27 and column 16, lines 29-32).

With regard to claim 74, Gordon teaches a method further comprising adding normal human nucleic acid to the single mixture to obtain heterozygous pairs, wherein

each heterozygous pair includes a normal segment of human nucleic acid and a mutated copy of the normal segment of human nucleic acid (mixture of DNA control construct can contain fragments that comprise wild-type sequence of interest and as many mutations and variations as desired, column 20, lines 48-51 and column 24, lines 26-42; mutations were added by site directed mutagenesis, column 27, lines 19-22).

Response to Arguments

5. Applicant's arguments filed September 21, 2006 have been fully considered but they are not persuasive.

Applicant argues that the 35 USC § 102(b) rejections of claims 1, 2, 4, 5, 7-9, 11, 16, 21-23, 28, and 71-74 as being anticipated by Chenchik et al. (U.S. Patent No. 5,759,822) and claims 1, 2, 4, 5, 8, 23, 71, and 72 as being anticipated by Legay et al. (Vet. Res. (2000) 31: 565-572) should be withdrawn since neither reference anticipates the claims as amended. Applicant argues that neither Chenchik nor Legay show or disclose synthesizing a clinically relevant reference nucleic acid in a base by base manner with one or more primer targets in the artificial base sequence for purposes of amplification. The Examiner disagrees that the Chenchik reference no longer meets the limitations of the claims as amended, and therefore maintains the rejections of claims 1, 2, 4, 5, 7-9, 11, 16, 21-23, and 71-74 as anticipated by Chenchik. However, the Examiner agrees that the Legay reference no longer anticipates the claims as amended and therefore the reference is withdrawn. In particular, Legay does not teach creating a clinical reference solution comprising a mutation in a human nucleic acid sequence isolated free from adjacent clinically irrelevant nucleic acid.

With regard to Chenchik, this reference teaches isolation of DNA fragments that can be used for co-amplification with normal DNA to measure the presence of differences between the sequences such as mutations, and therefore these fragments can serve as clinical references. The fragments can be prepared free of irrelevant DNA as cDNAs lacking non-cDNA sequences and other unrelated sequences. The fragments can be extended to create primer sites useful in amplifications. The fragments are generally created as PCR fragments, or can be fragments obtained from genomic DNA by random shearing or restriction endonuclease digestion, any of which were originally synthesized in a base by base manner. Finally, the fragments can form mixtures such as a cDNA library cloned into a vector and thus can be used in a multiplex format.

Upon further searching, another reference was found that also anticipates the claims as amended. Therefore, claims 1, 2, 4, 5, 7-9, 11, 16, 21-23, and 71-74 are rejected under 35 U.S.C. 102(a) as being anticipated by Gordon et al. (U.S. Patent No. 6,607,911). Gordon teaches the limitations of claim 1 for making control DNA constructs containing one or more clinically relevant sites in a base-by-base manner, wherein the construct contains one or more primer targets. Gordon also teaches the limitations of claim 71 for making multiple control DNA constructs, each with unique priming sites for use in amplification. Gordon also teaches the limitations of the dependent claims as presented above and therefore anticipates all of the claims as amended.

Summary

6. Claims 1, 2, 4, 5, 7-9, 11, 16, 21-23, and 71-74 are rejected. No claims are allowable.

Conclusion

7. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Correspondence

8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to David C. Thomas whose telephone number is 571-272-3320. The examiner can normally be reached on 5 days, 9-5:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on 571-272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

David C. Thomas 11/22/06

David C. Thomas
Patent Examiner
Art Unit 1637

JEFFREY FREDMAN
PRIMARY EXAMINER
11/21/06